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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/922,067

DATE: 11/19/2001

TIME: 09:46:22

Input Set : N:\Crf3\RULE60\09922067.raw

Output Set: N:\CRF3\11192001\I922067.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: MacPhee, Colin Houston

6 Tew, David Graham

7 Southan, Christopher Donald

8 Hickey, Dierdre Mary Bernadette

9 Gloger, Israel Simon

10 Lawrence, Geoffrey Mark Prouse

11 Rice, Simon Quentyn John

13 (ii) TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
14 Thereof And Use Of The Same In Diagnosis And Therapy

16 (iii) NUMBER OF SEQUENCES: 11

18 (iv) CORRESPONDENCE ADDRESS:

19 (A) ADDRESSEE: SmithKline Beecham Corporation

20 (B) STREET: 709 Swedeland Road

21 (C) CITY: King of Prussia

22 (D) STATE: PA

23 (E) COUNTRY: USA

24 (F) ZIP: 19406

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Diskette

28 (B) COMPUTER: IBM PC compatible

29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

32 (vi) CURRENT APPLICATION DATA:

C--> 33 (A) APPLICATION NUMBER: US/09/922,067

C--> 34 (B) FILING DATE: 03-Aug-2001

35 (C) CLASSIFICATION:

37 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: 09/193,130

39 (B) FILING DATE: 1998-11-17

41 (A) APPLICATION NUMBER: PCT/GB94/01374

42 (B) FILING DATE: 24 June 1994

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Dustman, Wayne J.

46 (B) REGISTRATION NUMBER: 33,870

47 (C) REFERENCE/DOCKET NUMBER: P30693

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 610-270-5023

51 (B) TELEFAX: 610-270-5090

52 (C) TELEX:

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 37 amino acids

58 (B) TYPE: amino acid

59 (C) STRANDEDNESS:

60 (D) TOPOLOGY: linear

ENTERED

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62      (ii) MOLECULE TYPE: peptide
64      (iii) HYPOTHETICAL: NO
C--> 68      (v) FRAGMENT TYPE: internal
70      (vi) ORIGINAL SOURCE:
C--> 72      (ix) FEATURE:
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76      Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu
77      1             5             10             15
79      Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
80      20             25             30
82      Lys Asp Phe Asp Gln
83      35
85 (2) INFORMATION FOR SEQ ID NO: 2:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 30 amino acids
89          (B) TYPE: amino acid
90          (D) TOPOLOGY: linear
92      (ii) MOLECULE TYPE: peptide
94      (iii) HYPOTHETICAL: NO
96      (v) FRAGMENT TYPE: internal
100     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
102     Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro
103     1             5             10             15
105     Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
106     20             25             30
108 (2) INFORMATION FOR SEQ ID NO: 3:
110     (i) SEQUENCE CHARACTERISTICS:
111         (A) LENGTH: 27 amino acids
112         (B) TYPE: amino acid
113         (D) TOPOLOGY: linear
115     (ii) MOLECULE TYPE: peptide
117     (iii) HYPOTHETICAL: NO
119     (v) FRAGMENT TYPE: internal
123     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
125     Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
126     1             5             10             15
128     Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
129     20             25
131 (2) INFORMATION FOR SEQ ID NO: 4:
133     (i) SEQUENCE CHARACTERISTICS:
134         (A) LENGTH: 19 amino acids
135         (B) TYPE: amino acid
136         (D) TOPOLOGY: linear
138     (ii) MOLECULE TYPE: peptide
140     (iii) HYPOTHETICAL: NO
142     (v) FRAGMENT TYPE: internal
146     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
148     Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
149     1             5             10             15

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151      Pro Ala Asn
154 (2) INFORMATION FOR SEQ ID NO: 5:
156      (i) SEQUENCE CHARACTERISTICS:
157          (A) LENGTH: 420 base pairs
158          (B) TYPE: nucleic acid
159          (C) STRANDEDNESS: double
160          (D) TOPOLOGY: linear
162      (ii) MOLECULE TYPE: cDNA
164      (iii) HYPOTHETICAL: NO
C--> 166      (iv) ANTI-SENSE: NO
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
172 AAAAAACCTA TTTTAATCCT AATTGTATTT CTCTATTCCT GAAGAGTTCT GTAACATGAT      60
174 GTGTTGATTG GTTGTGTAA TGTGGTCCC TGGAATAAGA TTCTCATCAT CTCCTTCAAT      120
176 CAAGCAGTCC CACTGATCAA AATCTTTATG AAGTCCTAAA TGCTTTTGTA AGAATGCTAA      180
178 TGAAGCTTTG TTGCTAAGAT CAATAGCTGC ATTTGAATCT ATGTCTCCCT TTAATTTGAG      240
180 CATGTGTCCA ATTATTTTGC CAGTNGCAA AGTGAAGTCA GCAAATTCCT GGTGGACTGA      300
182 ACCCCTGATT GTAATCATCT TTCTTTCTTT ATCAGGTGAG TAGCATTTT TCATTTTAT      360
184 GATATTAGCA GGATATTGGA AATATTCAGN GTTGNTAAAA AGNGGNGGCT GAGGGATTCT      420
187 (2) INFORMATION FOR SEQ ID NO: 6:
189      (i) SEQUENCE CHARACTERISTICS:
190          (A) LENGTH: 379 base pairs
191          (B) TYPE: nucleic acid
192          (C) STRANDEDNESS: double
193          (D) TOPOLOGY: linear
195      (ii) MOLECULE TYPE: cDNA
197      (iii) HYPOTHETICAL: NO
C--> 199      (iv) ANTI-SENSE: NO
203      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
205 TGCTAATATC ATAAAAATGA AAAAATGCTA CTCACCTGAT AAAGAAAGAA AGATGATTAC      60
207 AATCAGGGGT TCAGTCCACC AGANTTTTGC TGACTTCACT TTTGCAACTG GCAAAATAAT      120
209 TGGACACATG CTCAAATTAA AGGGAGACAT AGATTCAAAT GTAGCTATTG ATCTTAGCAA      180
211 CAAAGCTTCA TTAGCATTTCT TACAAAAGCA TTTAGGACTT CATAAAGATT TTGTTTCAGTG      240
213 GGACTGCTTG ATTGAAGGAG ATGATGAGAA TCTTATTCCA GGGACCAACA TTAACACAAC      300
215 CAATTCAACA CATCATGTTT ACAGAACTTC TTCCAGGGAA TAGGAGGAAA TACAATTGGG      360
217 GTTTAAAATA GGTTTTTTTT
219 (2) INFORMATION FOR SEQ ID NO: 7:
221      (i) SEQUENCE CHARACTERISTICS:
222          (A) LENGTH: 279 base pairs
223          (B) TYPE: nucleic acid
224          (C) STRANDEDNESS: double
225          (D) TOPOLOGY: linear
227      (ii) MOLECULE TYPE: cDNA
229      (iii) HYPOTHETICAL: NO
C--> 231      (iv) ANTI-SENSE: NO
235      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
237 GAAGAATGCA TTAGATTTAA AGTTTGATAT GGAACAACCTG AAGGACTCTA TTGATAGGGA      60
239 AAAAATAGCA GTAATTGGAC ATTCTTTTGG TGGAGCAACG GTTATTCAGA CTCTTAGTGA      120
241 AGATCAGAGA TTCAGATGTG GTATTGCCCT GGATGCATGG ATGTTTCCAC TGGGTGATGA      180
243 AGTATATTCC AGAATTCCTC AGCCCCTCTT TTTTATCAAC TCTGAATATT TCCAATATCC      240

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245 TGCTAATATC ATAAAAANTGG AAAAATGCTA CTCACCTGG
247 (2) INFORMATION FOR SEQ ID NO: 8:
249     (i) SEQUENCE CHARACTERISTICS:
250         (A) LENGTH: 572 base pairs
251         (B) TYPE: nucleic acid
252         (C) STRANDEDNESS: double
253         (D) TOPOLOGY: linear
255     (ii) MOLECULE TYPE: cDNA
257     (iii) HYPOTHETICAL: NO
C--> 259     (iv) ANTI-SENSE: NO
263     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
265 AAAATAGCAG TAATTGGACA TTCTTTAGGT GGAGCAACGG TTATTCAGAC TCTTAGTGAA      60
267 GATCAGAGAT TCAGATGTGG TATTGCCCTG GATGCATGGA TGTTCCTACT GGGTGATGAA      120
269 GTATATTCCA GAATTCCTCA GCCCCTCTTT TTTATCAACT CTGAATATTT CCAATATCCT      180
271 GCTAATATCA TAAAAATGAA AAAATGCTAC TCACCTGATA AAGAAAGAAA GATGATTACA      240
273 ATCAGGGGTT CAGTCCACCA GAATTTTGCT GACTTCACTT TTGCAACTGG CAAAATAATT      300
275 GGACACATGC TCAAATTAAA GGGAGACATA GATTCAAATG TAGCTATTGA TCTTAGCAAC      360
277 AAAGCTTCAT CAGCATTCTT ACAAAGCAT TTAGGACTTC ATAAAGATTG TGATCAGTGG      420
279 GACTGCTTGA TTGAAGGAGA TGATGAGAAT CTTATTCCAG GGACCAACAT TAACACAACC      480
281 AATCAACACA TCATGTTACA GAACTCTTCA GGAATAGAGA AATACAATTA GGATTAAAT      540
283 AGGTTTTTTT AAAAAAAAAA AAAAAAACT CG      572
285 (2) INFORMATION FOR SEQ ID NO: 9:
287     (i) SEQUENCE CHARACTERISTICS:
288         (A) LENGTH: 1361 base pairs
289         (B) TYPE: nucleic acid
290         (C) STRANDEDNESS: double
291         (D) TOPOLOGY: linear
293     (ii) MOLECULE TYPE: cDNA
295     (iii) HYPOTHETICAL: NO
C--> 297     (iv) ANTI-SENSE: NO
300     (ix) FEATURE:
301         (A) NAME/KEY: CDS
302         (B) LOCATION: 38..1360
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
307 TGAGAGACTA AGCTGAAACT GCTGCTCAGC TCCCAAG ATG GTG CCA CCC AAA TTG      55
308                                     Met Val Pro Pro Lys Leu
309                                     1           5
311 CAT GTG CTT TTC TGC CTC TGC GGC TGC CTG GCT GTG GTT TAT CCT TTT      103
312 His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
313         10           15           20
315 GAC TGG CAA TAC ATA AAT CCT GTT GCC CAT ATG AAA TCA TCA GCA TGG      151
316 Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
317         25           30           35
319 GTC AAC AAA ATA CAA GTA CTG ATG GCT GCT GCA AGC TTT GGC CAA ACT      199
320 Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
321         40           45           50
323 AAA ATC CCC CGG GGA AAT GGG CCT TAT TCC GTT GGT TGT ACA GAC TTA      247
324 Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
325 55           60           65           70

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327	ATG	TTT	GAT	CAC	ACT	AAT	AAG	GGC	ACC	TTC	TTG	CGT	TTA	TAT	TAT	CCA	295
328	Met	Phe	Asp	His	Thr	Asn	Lys	Gly	Thr	Phe	Leu	Arg	Leu	Tyr	Tyr	Pro	
329					75					80						85	
331	TCC	CAA	GAT	AAT	GAT	CGC	CTT	GAC	ACC	CTT	TGG	ATC	CCA	AAT	AAA	GAA	343
332	Ser	Gln	Asp	Asn	Asp	Arg	Leu	Asp	Thr	Leu	Trp	Ile	Pro	Asn	Lys	Glu	
333				90					95					100			
335	TAT	TTT	TGG	GGT	CTT	AGC	AAA	TTT	CTT	GGA	ACA	CAC	TGG	CTT	ATG	GGC	391
336	Tyr	Phe	Trp	Gly	Leu	Ser	Lys	Phe	Leu	Gly	Thr	His	Trp	Leu	Met	Gly	
337			105					110					115				
339	AAC	ATT	TTG	AGG	TTA	CTC	TTT	GGT	TCA	ATG	ACA	ACT	CCT	GCA	AAC	TGG	439
340	Asn	Ile	Leu	Arg	Leu	Leu	Phe	Gly	Ser	Met	Thr	Thr	Pro	Ala	Asn	Trp	
341		120					125						130				
343	AAT	TCC	CCT	CTG	AGG	CCT	GGT	GAA	AAA	TAT	CCA	CTT	GTT	GTT	TTT	TCT	487
344	Asn	Ser	Pro	Leu	Arg	Pro	Gly	Glu	Lys	Tyr	Pro	Leu	Val	Val	Phe	Ser	
345	135					140					145					150	
347	CAT	GGT	CTT	GGG	GCA	TTC	AGG	ACA	CTT	TAT	TCT	GCT	ATT	GGC	ATT	GAC	535
348	His	Gly	Leu	Gly	Ala	Phe	Arg	Thr	Leu	Tyr	Ser	Ala	Ile	Gly	Ile	Asp	
349				155					160					165			
351	CTG	GCA	TCT	CAT	GGG	TTT	ATA	GTT	GCT	GCT	GTA	GAA	CAC	AGA	GAT	AGA	583
352	Leu	Ala	Ser	His	Gly	Phe	Ile	Val	Ala	Ala	Val	Glu	His	Arg	Asp	Arg	
353				170					175					180			
355	TCT	GCA	TCT	GCA	ACT	TAC	TAT	TTC	AAG	GAC	CAA	TCT	GCT	GCA	GAA	ATA	631
356	Ser	Ala	Ser	Ala	Thr	Tyr	Tyr	Phe	Lys	Asp	Gln	Ser	Ala	Ala	Glu	Ile	
357			185					190						195			
359	GGG	GAC	AAG	TCT	TGG	CTC	TAC	CTT	AGA	ACC	CTG	AAA	CAA	GAG	GAG	GAG	679
360	Gly	Asp	Lys	Ser	Trp	Leu	Tyr	Leu	Arg	Thr	Leu	Lys	Gln	Glu	Glu	Glu	
361		200					205					210					
363	ACA	CAT	ATA	CGA	AAT	GAG	CAG	GTA	CGG	CAA	AGA	GCA	AAA	GAA	TGT	TCC	727
364	Thr	His	Ile	Arg	Asn	Glu	Gln	Val	Arg	Gln	Arg	Ala	Lys	Glu	Cys	Ser	
365	215					220					225					230	
367	CAA	GCT	CTC	AGT	CTG	ATT	CTT	GAC	ATT	GAT	CAT	GGA	AAG	CCA	GTG	AAG	775
368	Gln	Ala	Leu	Ser	Leu	Ile	Leu	Asp	Ile	Asp	His	Gly	Lys	Pro	Val	Lys	
369				235					240						245		
371	AAT	GCA	TTA	GAT	TTA	AAG	TTT	GAT	ATG	GAA	CAA	CTG	AAG	GAC	TCT	ATT	823
372	Asn	Ala	Leu	Asp	Leu	Lys	Phe	Asp	Met	Glu	Gln	Leu	Lys	Asp	Ser	Ile	
373				250					255					260			
375	GAT	AGG	GAA	AAA	ATA	GCA	GTA	ATT	GGA	CAT	TCT	TTT	GGT	GGA	GCA	ACG	871
376	Asp	Arg	Glu	Lys	Ile	Ala	Val	Ile	Gly	His	Ser	Phe	Gly	Gly	Ala	Thr	
377			265					270					275				
379	GTT	ATT	CAG	ACT	CTT	AGT	GAA	GAT	CAG	AGA	TTC	AGA	TGT	GGT	ATT	GCC	919
380	Val	Ile	Gln	Thr	Leu	Ser	Glu	Asp	Gln	Arg	Phe	Arg	Cys	Gly	Ile	Ala	
381			280				285						290				
383	CTG	GAT	GCA	TGG	ATG	TTT	CCA	CTG	GGT	GAT	GAA	GTA	TAT	TCC	AGA	ATT	967
384	Leu	Asp	Ala	Trp	Met	Phe	Pro	Leu	Gly	Asp	Glu	Val	Tyr	Ser	Arg	Ile	
385	295					300					305					310	
387	CCT	CAG	CCC	CTC	TTT	TTT	ATC	AAC	TCT	GAA	TAT	TTC	CAA	TAT	CCT	GCT	1015
388	Pro	Gln	Pro	Leu	Phe	Phe	Ile	Asn	Ser	Glu	Tyr	Phe	Gln	Tyr	Pro	Ala	
389				315					320					325			
391	AAT	ATC	ATA	AAA	ATG	AAA	AAA	TGC	TAC	TCA	CCT	GAT	AAA	GAA	AGA	AAG	1063

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09922067.raw

Output Set: N:\CRF3\11192001\I922067.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:66 M:220 C: Keyword misspelled or invalid format, [(v) FRAGMENT TYPE:]
L:72 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:166 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:199 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:231 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:259 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:297 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]